RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/603,138_
Source: _OIPE_
Date Processed by STIC: _7/30/2003_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 4.0 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> __http://www.uspto.gov/web/offices/pac/checker__

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<__http://www.uspto.gov/ebc/efs/downloads/documents.htm__>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
      Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary
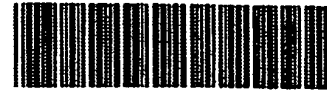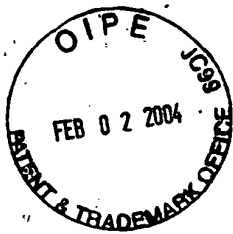
ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/603,138_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ Patentin 2.0
"bug"

A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ____. Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 __✓__ Skipped Sequences
(NEW RULES)

Sequence(s) _846 7_ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ Patentin 2.0
"bug"

Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 07/31/2003
PATENT APPLICATION: US/10/603,138   TIME: 07:45:01

Input Set : N:\DA\pto.da.txt
Output Set: N:\CRF4\07312003\J603138.raw

```
    3 <110> APPLICANT: Cathy Lofton-Day
    4    .     Andrew Sledziewski
    5          Jorn Lewin
    6          Fabian Model
    7          Tamas Rujan
    9 <120> TITLE OF INVENTION: Methods and nucleic acids for analyses of colorectal cell
proliferative
   10          disorders.
   12 <130> FILE REFERENCE: 47675-47
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/603,138     result of
C--> 14 <141> CURRENT FILING DATE: 2003-06-23             many duplicated sequences
E--> 14 <160> NUMBER OF SEQ ID NOS: 8475  8865
                    (see p.5)
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
E--> 31223 <210> SEQ ID NO: 1186 (see p.2)
E--> 35524 <210> SEQ ID NO: 1578
    111365 <210> SEQ ID NO: 8467
    111366 <211> LENGTH: 0                        delete all this
    111367 <212> TYPE: DNA
    111368 <213> ORGANISM: Artificial Sequence
    111370 <220> FEATURE:
    111371 <223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
    111373 <400> SEQUENCE: 8467
E--> 111375      000 (insert)
```

(if the above sequence is intentionally skipped, or delete
please use format shown in item 8 of Error
Summary Sheet)

```
<210> 1577
<211> 22
<212> DNA
<213> Artificial Sequence
<220> bisulfite treated    move this to <223> line (do not show any response
<223> nucleic acid for analysis of methylation status of SEQ ID NO: 27    to <220>)
<400> 1577
TATACGCGAT TTACGGTAGA GG          duplicate (already shown in file)    22
<210> 1186
<211> 22
<212> DNA
<213> Artificial Sequence
<220> bisulfite treated    same error
<223> nucleic acid for analysis of methylation status of SEQ ID NO: 4
<400> 1186
AGTTTCGCGG TTTATAGAGG TT                              22
<210> 1187    duplicate (already shown)
<211> 22
        ( many sequences duplicated )
        after 1186 above
```

This error begins with sequence 1160 (appears in many subsequent sequences)

```
<210> 1160
<211> 18
<212> DNA
<213> Artificial Sequence

<220> (bisulfite treated)  move to <2237 line  do not show any response to <2207. It is a "header" only.
<223> nucleic acid for analysis of methylation status of SEQ ID NO 16.
<400> 1160
(GGTTTCGGTT CGAGGTTC)                                              18
```

use only lower-case letters for nucleotides, when Sequence Listing is in new Sequence Rules format.

(Please edit all sequences showing upper-case letters for nucleotides)

<210> 536
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for what? (This is a sample of global error)

<400> 536

```
<210> 8474
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 8474

attaatggtt ttataagacg gatttttttt taacgt                      36
```

FYI: last sequence in submitted file, not 8475, as shown on p. 1 in 1607 response

FYI Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

Input Set : N:\DA\pto.da.txt
Output Set: N:\CRF4\07312003\J603138.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2936 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:2100
L:11560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:404 after pos.:2100
L:11580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:405 after pos.:60
L:18394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:520 after pos.:2100
L:18414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:521 after pos.:60
L:26628 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26631 M:112 C: (48) String data converted to lower case,
L:26639 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26642 M:112 C: (48) String data converted to lower case,
L:26650 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26653 M:112 C: (48) String data converted to lower case,
L:26661 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26664 M:112 C: (48) String data converted to lower case,
L:26672 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26675 M:112 C: (48) String data converted to lower case,
L:26683 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26686 M:112 C: (48) String data converted to lower case,
L:26694 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26697 M:112 C: (48) String data converted to lower case,
L:26705 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26708 M:112 C: (48) String data converted to lower case,
L:26716 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26719 M:112 C: (48) String data converted to lower case,
L:26727 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26730 M:112 C: (48) String data converted to lower case,
L:26738 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26741 M:112 C: (48) String data converted to lower case,
L:26749 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26752 M:112 C: (48) String data converted to lower case,
L:26760 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26763 M:112 C: (48) String data converted to lower case,
L:26771 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26774 M:112 C: (48) String data converted to lower case,
L:26782 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26785 M:112 C: (48) String data converted to lower case,
L:26793 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26796 M:112 C: (48) String data converted to lower case,
L:26804 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26807 M:112 C: (48) String data converted to lower case,
L:26815 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26818 M:112 C: (48) String data converted to lower case,
L:26826 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26829 M:112 C: (48) String data converted to lower case,
L:26837 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26840 M:112 C: (48) String data converted to lower case,
L:26848 M:256 W: Invalid Numeric Header Field, <220> has non-blank data

```
L:26851 M:112 C: (48) String data converted to lower case,
L:26859 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26862 M:112 C: (48) String data converted to lower case,
L:26870 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26873 M:112 C: (48) String data converted to lower case,
L:26881 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26884 M:112 C: (48) String data converted to lower case,
L:26892 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26895 M:112 C: (48) String data converted to lower case,
L:26903 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26906 M:112 C: (48) String data converted to lower case,
L:26915 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26918 M:112 C: (48) String data converted to lower case,
L:26926 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26929 M:112 C: (48) String data converted to lower case,
L:26937 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26940 M:112 C: (48) String data converted to lower case,
L:26948 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26951 M:112 C: (48) String data converted to lower case,
L:26959 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26962 M:112 C: (48) String data converted to lower case,
L:26970 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26973 M:112 C: (48) String data converted to lower case,
L:26981 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26984 M:112 C: (48) String data converted to lower case,
L:26992 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26995 M:112 C: (48) String data converted to lower case,
L:27003 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27006 M:112 C: (48) String data converted to lower case,
L:27014 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27017 M:112 C: (48) String data converted to lower case,
L:27025 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27028 M:112 C: (48) String data converted to lower case,
L:27036 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27039 M:112 C: (48) String data converted to lower case,
L:27047 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27050 M:112 C: (48) String data converted to lower case,
L:27058 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27061 M:112 C: (48) String data converted to lower case,
L:27069 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27072 M:112 C: (48) String data converted to lower case,
L:27080 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27083 M:112 C: (48) String data converted to lower case,
L:27091 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27094 M:112 C: (48) String data converted to lower case,
L:27102 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27105 M:112 C: (48) String data converted to lower case,
L:27113 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27116 M:112 C: (48) String data converted to lower case,
```

VERIFICATION SUMMARY   DATE: 07/31/2003
PATENT APPLICATION: US/10/603,138 TIME: 07:45:10

Input Set : N:\DA\pto.da.txt
Output Set: N:\CRF4\07312003\J603138.raw

L:27124 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27127 M:112 C: (48) String data converted to lower case,
L:27135 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27138 M:112 C: (48) String data converted to lower case,
L:27146 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27149 M:112 C: (48) String data converted to lower case,
L:27157 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27160 M:112 C: (48) String data converted to lower case,
L:27168 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27171 M:112 C: (48) String data converted to lower case,
L:31223 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 1186
L:35524 M:214 E: (33) Seq.# missing, SEQ ID NO:1577
L:111375 M:301 E: (44) No Sequence Data was Shown, SEQ ID:8467
L:14 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (8475) Counted (8865)